

	Query Match	56.2%	Score 443.4	DB 5	Length 5910
	Best Local Similarity	72.6%	Pred. No. 9.3e106		
	Matches 573	Conservative 0	Mismatches 216	Indels 0	Gaps 0
QY	1	tatgacatcggaagagagctggaggtgcccagttgcattccatcgttaagaagtgcccgagag	60		
Db	373	tacgaacccgagcaggaactctggcagtttgacagtttgcgtgtgttaagaatagcgcgtgag	432		
QY	61	aagaagcacggggcgttgaglatagcaacgaatgtaacatcaagaagcggcgagcggagc	120		
Db	433	aaaagtaccggtccctccaglatgcccgaatctcaatcaagaagaagagactaagtcagc	492		
QY	121	cggcgcggtgtgtgagccggagagagatacgagcgggaggttgagatcctcgcgagtgctg	180		
Db	493	cggcggggtgtgagccggagagacatacgagcggggaggttcaagatctctgaagaagagatccag	552		
QY	181	caccacaattgcatcatagcgttcgacaggtctcttgagaaacggcagcgagctgtgacatcc	240		
Db	553	caccacaattgcatcatcacccttgacagagctcttgagaaacgaagacgtcatccgtgacc	612		
QY	241	cttgagctagtgcttcggagagagctcttcgattctccctggcccaagaagagtcacatgagt	300		
Db	613	ttggaacctgltgcagcgtggcgagctgtttgactctcttagcgtgaagaagaactttaact	672		
QY	301	gagagagagcgccacaacgcttcaatgaagcagatcctgtagtgggtgtaactatccacaca	360		
Db	673	gaagagagagcgaactgtaattcttcaacaacattctaagtggtttacttaccctgcctcc	732		
QY	361	aagaaattgctcactttgattcgaagcagaaacatatagttctgttagacagaatatt	420		

Dh 733 ctcaaatcgccaccttgatctaaagcctgagacataaagctttgtatagaatgtc 792
Qy 421 cccattccacacatcaagcgtgatctgacttgcttgctcgaagaatagaatgagt 480
Dh 793 cccaacactcgatcaagaatgatcatctgacttgggttggccataaattgactttgaaat 852
Qy 481 gaatttaagaatatttttgggaagccggaatttgcttcacagaatgtgaaactcgag 540
Dh 853 gaatttaaaacatatttggaccctcgagttgtcgtcctctgagtagcaactatgaa 912
Qy 541 cccctgggtctgaggtctgacatgttgagataggcgctacaccacatcctcttaagt 600
Dh 913 cctcttgcttgtagagagatagtgagagcatcggggtatataacatctcctcctaagt 972
Qy 601 ggaagatccctctccttgaggagacaggaacaggaacactggaacataatcaatcagtg 660
Dh 973 ggggcccctccatctcttgtagacactaaagaaacgtttagcaatgataccgtctgc 1032
Qy 661 agttacgactttgatgagatctctcagccatacagagcgagctggccaagacttatt 720
Dh 1033 aactacgaatttgaagatgatacttcaagtaataccagtgccctagccaagattcata 1092
Qy 721 cggaaagcttctgttaaaagaccggaacgctcacacatacagaagagctctcagacg 780
Dh 1093 agaagacttctgttcaagatccaaagaaagaaatgacaattcaagatattgacagat 1152
Qy 781 cccttgatc 789
Dh 1153 cccttgatc 1161

RESULT 2

US-10-105-299-15131
; Sequence 15131: Application US/10105299
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 15131
; LENGTH: 12638
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-15131

Query Match 31.0%; Score 244.6; DB 6; Length 12638;
Best Local Similarity 79.6%; Pred. No. 4.3e-54;
Matches 289; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

Qy 25 agtggcaggttggcatcgtgaagaagtgcgcggagagaagacggyggttgatgca 84
Dh 6096 agcgagcaggttggcatcgtgagaaagtgcgcggagagaagacggyggttgatgca 84
Qy 85 gccaaattcatcaagaagcgcagagcgcgagccggcgcggttggagccggagag 144
Dh 6156 gccaaattcatcaagaagcgcgcgcctgtcatccagccggcgcggttggagccggagag 144
Qy 145 atcgagcgagagtgagcatcctcgcgaggtgctgcacacaaatgtcatcagcgagc 204
Dh 6316 atcgagcgagagtgagcatcctcgcgaggtgctgcacacaaatgtcatcagcgagc 204
Qy 205 gacgtcatatgaagacccagcagcgtggtgcatatccttgagttaatgtctggagagag 264
Dh 6276 gacatctctgagaaagaaagagcgtggtctcatcctcctgagatggttcttgcgagag 6335
Qy 265 ctcttgatctctgcccagaaagagtcactgtagtgaagagagccacaggttcatc 324
Dh 6336 ctcttgatctctgcccagaaagagtcgtcgtgagagagagccacaggttctc 6395

Qy 325 aagcagatcttgatgaggtgagtaactacatccacaaagaatgtcacttgatctc 384
Dh 6396 aagcagatcttgagagcggttcaactacatccatgaagcagatcgcaacttgaact 6455
Qy 385 aag 387
Dh 6456 aag 6458

RESULT 3

US-09-966-607-12
; Sequence 12: Application US/09966607
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN KINASE AND
; FILE REFERENCE: NMI-196
; CURRENT APPLICATION NUMBER: US/09/966,607
; CURRENT FILING DATE: 2002-04-18
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 12
; LENGTH: 1449
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 249
; OTHER INFORMATION: n=any nucleotide
US-09-966-607-12

Query Match 23.7%; Score 187.2; DB 5; Length 1449;
Best Local Similarity 56.0%; Pred. No. 2e-39;
Matches 432; Conservative 0; Mismatches 313; Indels 27; Gaps 3;

Qy 20 ttggagtgagccagtttgccatcgtgaagaagtgcggagaaagacacgggctgagtc 79
Dh 617 ttggagtgagcggttccgcgcaggttccacaaagtgtgaagagcgcacaaagcttgaagc 676
Qy 80 atgcagccaaattcatcaagaagcgcagagccggcgagccggctgtgagccggg 139
Dh 677 tggcagccaaatcatcaagaagcgcagagccggcgagccggctgtgagccggg 139
Qy 140 agagatcgagcgagagtgagcatccttgcgaggtgctgcacacaaatgtcatcagc 199
Dh 719 agagagtgagaaagacgagatcagcgttcatgaaccagcttgacacagacccatccagc 778
Qy 200 tgcagagctcatgagaaacgcagcagcgtgtgtcacatccttgagctagtgctgag 259
Dh 779 tgcagatgctctcgagtgctaaagacatgtctcgtgtcatgagatgtgagtggtg 838
Qy 260 gaggagcttga-----ttcctggcccgagaaagagtcactgagtgagagagagccacca 316
Dh 839 gggagctgttttaccgcgacacatcgatgagagctacaatttgaacgagcttgatcacacc 898
Qy 317 gcttataaagagatctctgagtgaggtggaactacatccacaaagaatgttgcact 376
Dh 899 tgttataagagagatgtgtaggggagtaagagcacatgacatgagatgtcatctccact 958
Qy 377 ttgatctaaagccgaaataatattgtgttagacaaagaatattccattccacacatca 436
Dh 959 tggagctgaagccctgagatatctcgttgtt-----gaatcgagatgctgaagaataa 1012
Qy 437 agctatgacttggcttggctcagaaatagaagatgaggttgatattagaatatct 496
Dh 1013 aaattattgattttgagatgtgcccagaagatatacaaacacagagaaagctgaagtgact 1072
Qy 497 ttggagcgccggaattgtgtgtccagaaatgtgaaactagaaagcccttggtctggag 556
Dh 1073 ttgaaacccagaaatttctcgcctcgaagtgtgaaactatgatttgttcatattcca 1132

[illegible]

```

RESULT 5
PCT-US02-10818-20
; Sequence 20, Application PC/TUS0210818
; GENERAL INFORMATION:
; APPLICANT: INCYTE GENOMICS, INC.
; APPLICANT: Recipon, Shirley A.
; APPLICANT: Burrill, John D.
; APPLICANT: Marcus, Gregory A.
; APPLICANT: Zingler, Kurt A.
; APPLICANT: Tang, Y. Tom
; APPLICANT: Thornton, Michael
; APPLICANT: Borowsky, Mark L.
; APPLICANT: Baughn, Mariah R.
; APPLICANT: Burford, Neil
; APPLICANT: Lee, Soo Yeun
; APPLICANT: Bandman, Olga
; APPLICANT: Hafalia, April J.A.
; APPLICANT: Yao, Monique G.
; APPLICANT: Rankumar, Jayalaxmi
; APPLICANT: Walla, Narinder K.
; APPLICANT: Lu, Dyung Aina M.
; APPLICANT: Arvizu, Chandra S.
; APPLICANT: Ison, Craig H.
; APPLICANT: Ding, Li
; APPLICANT: Lu, Yan
; APPLICANT: Gurturajan, Rajagopal
; APPLICANT: Walsh, Roderick T.
; APPLICANT: Gandhi, Ameena R.
; APPLICANT: Swarnakar, Anita
; APPLICANT: Forsythe, Ian J.
; APPLICANT: Yue, Henry
; APPLICANT: Au-Young, Janice K.
; APPLICANT: Elliott, Vicki S.
; APPLICANT: Lee, Sally
; TITLE OF INVENTION: KINASES AND PHOSPHATASES
; FILE REFERENCE: PI-0398 PCT
; CURRENT APPLICATION NUMBER: PCT/US02/10818
; CURRENT FILING DATE: 2002-04-05
; PRIOR APPLICATION NUMBER: 60/282,119; 60/283,588; 60/283,759; 60/285,589; 60/287,461; 60/287,036; 60/288,608; 60/288,712; 60/289,909; 60/292,246
; PRIOR FILING DATE: 2001-04-06; 2001-04-13; 2001-04-13; 2001-04-20; 2001-04-27;
; 2001-04-27; 2001-05-04; 2001-05-04; 2001-05-09; 2001-05-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PERL Program
; SEQ ID NO 20
; LENGTH: 2386
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

```

```
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No: 7472696CB1
PCT-US02-10818-20
```

Query Match	23.58;	Score 185.6;	DB 1;	Length 2386;
Best Local Similarity	55.68;	Pred. NO. 5.8e-39;		
Matches 434;	Conservative 0;	Mismatches 319;	Indels 27;	Gaps 3;

[illegible]

```

? PRIOR APPLICATION NUMBER: 60/129,533
? PRIOR FILING DATE: 1999-04-16
? NUMBER OF SEQ ID NOS: 17
? SOFTWARE: FastSeq for Windows Version 4.0.
? SEQ ID NO 3
? LENGTH: 5007
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: CDS
? LOCATION: (97)..(4926)
US-03-548-473b-3

```

Query Match	16.0%;	Score 126.2;	DB 5;	Length 5007;
Best Local Similarity	49.9%;	Pred. No. 1.8e-23;		
Matches 394;	Conservative 0;	Mismatches 368;	Indels 27;	Gaps 21;

QY	1	taagacatctcggagagagctctgggagatgagccagattctgcacatctctgtaagaagatgctccggagag	60
Db	424	tatcgatgacaaagagaaagatcttgaaaggggctggtcttgctcttaaaagaagatgctgagccac	483
QY	61	aagagacacggggctctgagatatactgacacaaattctacataagaagagcggagacagccgggagagc	120
Db	484	aaaggaagaacaaagatctcttgctgctgcgcacaaagtacatccctctaaaggggcga-----	534
- QY	121	cggcgggctgtgagccgggagagagatcagagccgggaggttgagagctacctgcgcgcagatgtgctg	180
Db	535	-----actcgggcgcacagacatacagggagagcagacatactctggccggcgctgagc	582
QY	181	caacacaaatgtctacatcacgctctgcacgaaagtctataagaaagacgcacccgagctggctgacacatc	240
Db	583	caaccccgctgacacaggggctgctgtagacaaattctgagagcccgccacagaacccctcacatcccttccac	642
QY	241	cttgagctaaagtgtctggaagagagctcttcgaattctccctggccacgaagagatctacatgagct	300
Db	643	ctggagctgagctgctacatccggagagagctctggaacccgtacagagagaggggcgtgtgacg	702
QY	301	gagggagggggcgcacacagctctcatatgaagacagatccctggagctggggtctgacatacttcaacaa	360
Db	703	gagggcggaggggcacaaagctctacacatcacagctctggtgaggggggtctgacatacttgcacagc	762
QY	361	aagaaaaatgtctacatcttctgaatctcaagacgaagaacaatatatgtctgtagacaagaataat	420
Db	763	catggcgtctctcacacctcggaataaagccctctcaacatccctgaatgtgct-----gatacct	816
QY	421	cccatctcacacacatcaagctcgtatgacttggctctgctgtccacgaaataagaaatgagat	480
Db	817	gcccggaggaacatataaacatctgcagactctgtgctcttggccagaaacatacaccacccagcagag	876
QY	481	gaatttaagaataattcttgggagccgggaattgtgtgctccacgaanaattgtgacatacagag	540
Db	877	ctgcagattcacgacagatcgggctccctctggaattctgctcccccgaagatcatctcacagaagac	936
QY	541	ccccctgggctctggaagctctgacatgtggagacatagagcgtatcacatcacatctcttaagt	600
Db	937	ccctggagcgaaagcctccgacacatttgggcatagtgggtacatctctactcactcagcctgacc	996
QY	601	ggagacatccctctccctcggggagagacagaaagcagaaacatctgccaataatacatcacatg	660
Db	997	tgtctacatcccatattgtccggagagatgagccgtgcacacctctctgaacgtctccctggaggg	1056
QY	661	agttacgaacttgatgagagatctctcacagccatacagagagctgacagagacttatct	720
Db	1057	cggctgctacatggggcagcccccatgctgtccacacctcctacagagagacgcacaaagactctac	1116
QY	721	cggaaagctcttggttaagaagacccggaaagcgtctcacacatcacaaagagctctcagaagac	780
Db	1117	aagcctacgctctgacagagagccctccagggcccgctcagtgctggcccaatgtctctccac	1176
QY	781	ccctcgatc	789
Db	1177	ccctcgatc	1185

```

RESULT 7
US-09-548-473B-5
: Sequence 5, Application US/09548473B
: GENERAL INFORMATION:
: APPLICANT: Wenlin Zeng
: APPLICANT: Lawrence Stanton
: APPLICANT: Haiyan Kong
: TITLE OF INVENTION: Mediators of signal transduction
: FILE REFERENCE: SCIOS.021A
: CURRENT APPLICATION NUMBER: US/09/548,473B
: CURRENT FILING DATE: 2000-04-13
: PRIORITY FILING DATE: 1999-04-16
: NUMBER OF SEQ ID NOS: 17
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 7928
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: CDS
: LOCATION: (60)...(7847)
: US-09-548-473B-5

```

Query Match	16.0%	Score 126.2	DB 5	Length 7928
Best Local Similarly	49.9%	Pred. NO. 2e-23		
Matches 394	Conservative	0	Mismatches 368	Indels 27
				Gaps 2

0Y	1	taibgcatacagagaaagatctggagggctggccagttcttcgatactgtgaagaagtgcgaggag	60
Db	3345	taacggatcgaagagaaatctggaaaggagcgatgtcttgcttgataaaagatgacac	3404
0Y	61	aagaaacagcgggctctgaaatctgaacacaaagtctcaacaaagaacggcagagccggagac	120
Db	3405	aagagaaacaaagatctctgctgcctgcaaaagtctcaatccccctacgagacga-----	3455
0Y	121	cggcgctgtctgagccggagagaaatctgaacggagggctgaaacatactctgcgacagtgtcgg	180
Db	3456	-----actccggcccaagacatacaagggagcgaaagatactcttgcgcgctgagac	3503
0Y	181	caacacaatgtcatcacatccgctgcagcagcgtctctatgtgaacacccagcagctggctgacatc	240
Db	3504	caaccgcctggtctaaacgggctcgtctgaaacaaagtctggagaccggaaaacctctactac	3563
0Y	241	cttgagctagtgctctgaaagaaagctctctcgattctcctggcccaagaagagtcaatgagt	300
Db	3564	ctggagcctgtgacataccgaaagagctgtgacacgcctgttaagaagaagcgctggtagacg	3623
0Y	301	gagggagggagccacaagactctatgaagcaagatccctcgagaggggtgaactacatctaca	360
Db	3624	gagggccggaggtcaaaagctctacatacgaacgacgtgtgtgaagggtctcacacacccgcagac	3683
0Y	361	aagaaaatgtctcaatcttgatctcaagccaaagaaaacataatgtctgaacaaagataat	420
Db	3684	catgctgtctctcaaccttgacataaagacctctaaacatctcgatgt-----gcatcct	3737
0Y	421	cccatctcaacatacaagctgtatgtactttgtctcggctcaacgaataatgaatgagt	480
Db	3738	gcccggagaaagaaatctaaactctgcgaatcttggctcttgcccaaaacataccccaagcagag	3797
0Y	481	gaatttaagaaatattctctggaacgcggaaatttgtctgcacgaagaattgtgaactacgag	540
Db	3798	ctgcagctcaagcagtaacgctccctcgtgtctctcccccagagatactccagcagaac	3857
0Y	541	ccccgggtcttgaaagctgacactggagacataggcgtatataccttactctcttaagt	600
Db	3858	ccctggagacgaagcctccgaacatctgggacatgggtgttaattccttaacctcagcctgac	3917
0Y	601	ggagatcccccttctcctggagacacgaagacgagaaacgtgccaatatctacatcatgt	660

Db	3918	tgctcatcccatcttgcggcgagagtgcacgtgcacccctctctaaagctctggaaggg	3977
Qy	661	agttacgactttgatgaggaattcttcacacatagcgaagctgycgaagactttat	720
Db	3978	cgcgltcatcagtagcagcccatctgctgcgccactcaggaagacgcgaagaacttcat	4037
Qy	721	cggaagctcttggttaagaagaccggaagaagcttcaatccaagaagctctcagaac	780
Db	4038	aagctacgctgcagagagccctccatgcccgcctatgctgcccagtgccctctccac	4097
Qy	781	ccctgatac	789
Db	4098	ccctgattc	4106

```

RESULT      8
US-09-053-375B-757
; Sequence 757, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chemchik, Alex
; APPLICANT: Biblashvilli, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CLON-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; CURRENT FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 757
;   LENGTH: 3165
;   TYPE: DNA
; ORGANISM: Mus musculus
US-09-053-375B-757

```

Query Match	15.3%	Score 120.6	DB 5	Length 3165
-Best Local Similarity	51.5%	Pred. No. 4.6e-22		
Matches 329	Conservative	0	Mismatches 324	Indels 6
				Gaps 2
QY 154	gaggtgagcaccctctgcggcaggctgctcagccaccatgtcatcagctgcagcgtctat	213		
DB 298	gaaatagaggtctctctgcgtctctctccaccccggaacatcataaactcaagaaatattc	357		
QY 214	gagaaaccgcagccagcgttggtcacatcccttgcagtagtctctcggaggaagctctcgat	273		
DB 358	gaaacccccacagaatacgaatcagcctgtctctcttgcgtctcgtgtcacagaggaggaactgtttgac	417		
QY 274	ttctctgcgccaaagagagtagtactgaagtgaaggagggccacagcttcattagcagatc	333		
DB 418	agagattgttgagaaagagatcacacagtagtgagcgcgatvgcgtgcagcgggttgagcagatc	477		
QY 334	ctggatctgggggtgaactactcttcacacaaagaaattgtccctactcttgatctaaagccaga	393		
DB 478	ctggagagccgctgtgcttaacctgtcaataatgtgagattgttcacgcggaacctcaaccagaag	537		
QY 394	aacattatctgtctcagacagaaatattccattccacacatcaagctgaattacttggat	453		
DB 538	aa-----tctctttagcaaatccagccctctgtgtgacacccctcaaaattgtcgaatttggaa	594		
QY 454	ctgctctacagaaatagaagaatgagatgtgaatttgaatlaagaalatcttctggagcgcggaattt	513		
DB 595	cttcaaaaattgttgaaacatcaagtgctcatgaaagacagtgctgttgaaaccccggtatc	654		
QY 514	gttgtctccagaattgttgactacagagcccccgggtctcgaagcgtcgacatgtggagacata	573		
DB 655	tcgcgaacctggaattctccgaggcgtgtgctactacggaacctggaagtcggaactgtgctctgaa	714		
QY 574	ggcgctacacacatacctctctccttaagtcgagagatcccccttctcgtggagacagaaacag	633		
DB 715	ggaataatacctacatacctactctgtgtgatttgaacctctatagaagcagagagtgat	774		
QY 634	gaaacacatggcaaatatacacatcagtgatgatttgcagcttgcattgtatgaagaaattcttcagc	690		
DB 775	cgctcatcttcaagagaaattctgaaatttgaattatctatctatctcccccggtggagat	834		

QY 631 catccgagcggcgccgcaagacttatctcggtaagagaccggaaa 750
Dd 835 gaagtgctttaaatacgcaagacttggccaagaacatgttttggatcccaagaa 894
QY 751 cggtcccaatcatccaagaggtctctcagaacaccctggaatc 789
Dd 895 cggtcgaactacattccaagccctccaacaccatggggtc 933

```

RESULT      9
PCT-US02-10786-1
: Sequence 1, Application PC/WTUS0210786
: GENERAL INFORMATION:
:   APPLICANT: LEXICON GENETICS INCORPORATED
:   TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
:   FILE REFERENCE: LEX-0332-PCr
:   CURRENT APPLICATION NUMBER: PCT/US02/10786
:   CURRENT FILING DATE: 2002-05-04
:   PRIOR APPLICATION NUMBER: US 60/282,036
:   PRIOR FILING DATE: 2001-04-06
:   NUMBER OF SEQ ID NOS: 6
:   SOFTWARE: FastSeq for Windows Version 4.0
:   SEQ ID NO 1
:   LENGTH: 2337
:   TYPE: DNA
:   ORGANISM: homo sapiens
PCT-US02-10786-1

```

Query Match	14.2%	Score 112;	DB 1;	Length 2337;
Best Local Similarity	52.6%	Pred. No. 7.2e-20;		
Matches 300;	Conservative 0;	Mismatches 255;	Indels 15;	Gaps 2

[illegible]

```

RESULT 10
US-10-116-326-1
; Sequence 1, Application US/10116326
; GENERAL INFORMATION:
; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Friddele, Carl Johan
; TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0332-USA
; CURRENT APPLICATION NUMBER: US/10/116,326
; CURRENT FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,036
; PRIOR FILING DATE: 2001-04-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2337
; TYPE: DNA
; ORGANISM: homo sapiens
US-10-116-326-1

```

Query Match	14.2%	Score 112;	DB 6;	Length 2337;
Best Local Similarity	52.6%;	Pred. No. 7.2e-20;		
Matches 300;	Conservative 0;	Mismatches 255;	Indels 15;	Gaps 2

QY	88	aaggtcattcaagaagacgagccagagccgggacggcgcgagctgtagagccgggagagatc	147
Db	175	aaggtccgcacatcaagatcgtgaaacccgggagaaagcctgtctggctcgtctgattgaagtgtg	234
QY	148	gagccggagagctgtagatctccctcggccagagctgtctgcacacaaatgtcatccacgtctgcagac	207
Db	235	gagcgtggagatcgcaccatctgaagctcatctgaacaacacacatgtccctcaagcttccacgac	294
QY	208	gtctattgagaaacgcgacccgagccgtgtgtgcatactcttgaagctagtctcttgagaggaagctc	267
Db	295	gtctccgagaaacaaagaaatatttctaacctgtcttgtagagcagctctcggggttgagctaa	354
QY	268	tctgaattccctcggcccaaaagagatctacctgtgtgtagaggaaggccacacagcttccattaag	327
Db	355	tctgcattccctcggctaaagaaaggagagactgcacgcgccaagagggccggaaggtcttcttcgc	414
QY	338	cagaatccctggaatgggtgtgaactacatccctcacacaaagaaagtctgcactcttgatctcaag	387
Db	415	cagatttgtctgcgtgcgtgactctctgcacacagctaccctccctctgcgcacagagaccctaaag	474
QY	388	cccaaaaaacattatgttgttgaagacaagaatatctccattccacacacatacaagctgattgac	447
Db	475	cccgagaaacctgctcttttggatgtagaataaataca-----acatccgcatgtgagac	522
QY	448	ttctgtctgctccagaaatatagaagatgaggttgaaatttaagaatatcttttggagccgg	507
Db	523	tctgcacatgcgtctccctgcgcagctgtgggagacagctctccttggagaccagctgtgcgtccccc	582
QY	508	gaatttgctgtctcaga---aattgttaacatacgaacccctgtgtcttgtagagctgacatg	564
Db	583	catatgcgtgtccacagaggtgattaaagggggaaaaatatgatabgccggccgggcagacatag	642
QY	565	tggagacatagggctacacatacctacatcctcttaagtgtgagacatcccttctcttgagagac	624
Db	643	tggagctgtgtagtcatcactccttcggccctcgtctcgtgggggtctctgcctttgatagcac	702
QY	625	acgaagacagagaaacactctgcgaatatcacaa	654
Db	703	aaactccgcacagctgctgtgagaaagctgtgaaa	732

RESULT 11
US-09-053-375B-171
; Sequence 171, Application US/09053375B
; GENERAL INFORMATION:

```

: APPLICANT: Cherkashin, Alex
: APPLICANT: Bibliashvili, Robert
: TITLE OF INVENTION: Nucleic Acid Arrays
: FILE REFERENCE: CLON-006
: CURRENT APPLICATION NUMBER: US/09/053,375B
: CURRENT FILING DATE: 1998-08-31
: NUMBER OF SEQ ID NOS: 1543
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 171
: LENGTH: 1640
: TYPE: DNA
: ORGANISM: Homo sapiens
US-09-053-375B-171

```

Query Match	13.9%	Score 109.4	DB 5	Length 1640
Best Local Similarity	50.4%	Pred. No. 3.1e-19		
Matches 322	Conservative 0	Mismatches 311	Indels 6	Gaps 2

QY	154	gaggttggagcattccgctcgaggtgtctgtgacacaaatgttcaacgcgtgcgcgcgtcat	213
Db	364	gagatagtagagattctctctctgtgcctctccacaccaaactttaaaacttaagaagatatt	423
QY	214	gagaaacgcacacgcagctgtgtgacatactctgtaggttagtctgtgagagagccttcgat	273
Db	424	gaaacccctacagaaatcagatctgtccttagaactctgtccagagagagacctgttgat	483
QY	274	ttctctgccccgaaagaggttccactgtagtgtagagagagagccacagcttcattaaagcagat	333
Db	484	aggaatctgtgaaaagagagatattacatgtgagcagagatgtctgcagatgtccgtttaaacaatc	543
QY	334	ctggatctgggtgtgaaactccctctccacacaaagaaatctgtcaacttgtatctcaagcgaa	393
Db	544	ctggagagcagttgtcttatctctacatgaaanaatgtgagatgtgtcatatcgtgtatcccaacagag	603
QY	394	aacatcatgtgtgttagagacagaaatattcccatctccacacatacaagctgtatgtactt	453
Db	604	aa----ctctctcttcttagaacctccagcccgccagatgtcacacactcaaaatctcgtattt	660
QY	454	ctggctctccagaaatagaaatgtgaggttctgaaattgaagatatatttttggagacgggaattc	513
Db	661	ctctcttaaaattgtgtgaaacatacaagatgtctcatgtgaagacagaaatgtgtgaacccaggtgac	720
QY	514	gttctccagaaatctgtgaaactaaagagacccctgtgtctgttggaggtcgtgacatgtgtgaagata	573
Db	721	tgtgcacacttgaaattctcttagaggtgtgtgtccatgtgaccttgagtggtgcagctgtgtcgtta	780
QY	574	ggcgatcatcacctcatctctctcttaagtgtgagacatcccttctcctgtggagacacgaagcag	633
Db	781	ggaaataaacctctcatctcttctcttctgtgtgaatttgaaacacttctatgtatgtgaaagagcgtat	840
QY	634	gaaacacatcggaataatcatcacatcagtgagtttagcgaacttggatgtgaagatattccttcagcat	693
Db	841	cagttcatgtctcagaggaatctcgtgaattgtgtgaatatattacttatctctccctgtgttgat	900
QY	694	acgagcgaagct--ggccaaaggaacttatctcggagaagcttctgtgttaaagagacccggaa	750
Db	901	gaaatctcttaaatgtccaaagacttgtgtcgaanaataatgtgtttgtgttccaaagaa	960
QY	751	cggtctacaaatccaaagaggtctctctagaacacccctgtgac	789
Db	961	cggtctacatcatcttcaagactctctcaagactcgtgtgtgtc	999

```

RESULT 12
PCT-US02-10786-5
: Sequence 5, Application PC/TUS0210786
: GENERAL INFORMATION:
: APPLICANT: LEXICON GENETICS INCORPORATED
: TITLE OR INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
: FILE REFERENCE: LEX-0332-PCt
: CURRENT APPLICATION NUMBER: PCT/US0210786
: CURRENT FILING DATE: 2002-05-04

```

```

? PRIOR APPLICATION NUMBER: US 60/282,036
? PRIOR FILING DATE: 2001-04-06
? NUMBER OF SEQ ID NOS: 6
? SOFTWARE: FASTSEQ for Windows Version 4.0.
? SEQ ID NO 5
? LENGTH: 2112
? TYPE: DNA
? ORGANISM: homo sapiens
? COT-0502-10786-5

```

Query Match	13.2%;	Score 103.8;	DB 1;	Length 2112;
Best Local Similarity	53.2%;	Pred. No. 9.4e-18;		
Matches 275;	Conservative	0;	Mismatches 227;	Indels 15; Gaps 2.

[illegible]

```

RESULT 13
US-10-116-326-5
: Sequence 5, Application US/10116326
: GENERAL INFORMATION:
: APPLICANT: Turner, C. Alexander Jr.
: APPLICANT: Mathur, Brian
: TITLE OF INVENTION: Novel Human Kinases and Polynucleotides Encoding the Same
: FILE REFERENCE: LEX-0332-USA
: CURRENT APPLICATION NUMBER: US/10/116,326
: CURRENT FILING DATE: 2002-04-04
: PRIOR APPLICATION NUMBER: US 60/282,036
: PRIOR FILING DATE: 2001-04-06
: NUMBER OF SEQ. ID NOS: 6
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ. ID NO 5
: LENGTH: 2112
: TYPE: DNA
: ORGANISM: homo sapiens
US-10-116-326-5

```

Query Match 13.2%; Score 103.8; DB 6; Length 2112;
Best Local Similarity 53.2%; Pred. No. 9.4e-18;
Matches 275; Conservative 0; Mismatches 227; Indels 15; Gaps 2;

QY 141 gggagatcgagcgaggtgtgcatctccgagcggtgtgtcaccacaattatcatcagct 200
DB 3 gaaagggtgagcgaggtgtgtcgcacatctgaagctcatcgaaccacattgtccctcagct 62
QY 201 gcaagcgtctatgaaagccgacccgagctgtgtgacatccttgagctagtgtctgagg 260
DB 63 ccagcagctctacgagacagaataattgtacctgtgtctgagagcgtcccgagg 122
QY 261 agagcctctgattctcctgtgcccagaagagtgactagtgtgagagagggccacagct 320
DB 123 tggagctatctgactactgtgtlaaagaaggagactgacgcccagaagggcccgaaagt 182
QY 321 catlaagacatctgagtgtgtgactccttcacacagaataattgtcatttga 380
DB 183 ctcccgccagatgtgtctgctgctgactctgtccacagctactcatctgtccacagaga 242
QY 381 tctcaagcagaataatattgtgtlaagacaagaatattccatccacacatacagct 440
DB 243 cctlaagcccgagacactgttltgtgtagaataaaca-----acatccgcat 290
QY 441 gattgacttgtgtctgtccacgaataagagatgtgaattgaataatttttg 500
DB 291 tgcagactctgcgactgtcctccctgcaggtgtgggagcagctcctgtgaagccagctgcyg 350
QY 501 gacgcggaattgtgtgtccagaataattgtgaactacgagccct---gggtctgagagc 557
DB 351 gtccccccttatgtgtctccagaggtgattaagggggaaataatgatgtggtccgagcggc 410
QY 558 tgaatgtgagcatagagcgatcatcctccttaagtgtgagcatcccttccct 617
DB 411 agacatgtgagctgtgtgagtgatcctcttcgcccgtcggtggggtcctgtccttga 470
QY 618 gggagacagaaagcggaacactgtgcaaatatcaca 654
DB 471 tgaagacaacactcgcagctgtgtgagaagtgtaa 507

RESULT 14
US-09-053-375B-774
; Sequence 774, Application US/09053375B
; GENERAL INFORMATION:
; APPLICANT: Chemchik, Alex
; APPLICANT: Bibilashvili, Robert
; TITLE OF INVENTION: Nucleic Acid Arrays
; FILE REFERENCE: CION-006
; CURRENT APPLICATION NUMBER: US/09/053,375B
; NUMBER OF SEQ ID NOS: 1543
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 774
; LENGTH: 3081
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-053-375B-774

Query Match 12.5%; Score 98.6; DB 5; Length 3081;
Best Local Similarity 49.5%; Pred. No. 2.3e-16;
Matches 319; Conservative 0; Mismatches 314; Indels 12; Gaps 2;

QY 157 gtgagcatcctgagcgaggtgtgtgacacacatgtcacagctgtcacgagctctatag 216
DB 1499 gagattctctgctgtatgctgacagaccacacatcatcaccctgtgaagaatggttgaac 1558
QY 217 aacgcgacgcgctgtgtacatctctgagctagtgtctgtgagagagagctcttcgattc 276
DB 1559 gatgtgaagcacgttactgtgtgacagagctgatgagggcgagagctgtgtgataag 1618

QY 277 ctggcccaagaggtactagtgtaggagggccacacattcatlaagacatctg 336
DB 1619 atcttaagcgagaaagctctcttcagagcggaagccagctctgtctgacacatcagc 1678
QY 337 gatgggttgaactactcttcacacaaagaaattctcaacttgaattctcaagccgaagaa 396
DB 1679 aagactgtgaatattgtcaactcctcaaggggtgtgtccacagagatctcaaaccaagta 1738
QY 397 attatgtgttgaagcaagaatattccattccacacatcaagctgtatgtactgtgtctg 456
DB 1739 atccctatgtgtgagtgctgtggaaaccgagtgctgtgcactgtgcactgtgtgtct 1798
QY 457 gtlcacaataa--gagagtgtgtgaatttaagaataatttttggagccgggaatt 513
DB 1799 gccaaagagatagggcgccggaagagctcctcatgtacactgtctacagccaactt 1858
QY 514 gtgtctcaagaatttgaactacgagccctgtgtgtgtgaggtgacatgtgagata 573
DB 1859 gtgtcactgtaggtctcctgaagcgccaggtgctagatgaaggtgtgtgacatgtgagcctg 1918
QY 574 ggcgtacacccatcactccttaagtgtgagatccctt-----ccttgagac 624
DB 1919 ggcattctgtgtacagatgtgtgcaggaalacactcattgtccaaatgtggccagtgac 1978
QY 625 accgaagcagaagaacactgtgcaaatatcacatcagtgtagttagactgtgtgaggaattc 684
DB 1979 accccagagagagatctccacccgagctgcagcggaagttcaaccctcaatgtggggaac 2038
QY 685 tttagccatacgagcgagctgtgccaaagacttaattcgaagctctctgtttaaagagac 744
DB 2039 tggaaacaggttctcaagaaagacgaagactgtgtatcaagtgtgtgactgtgtgagccc 2098
QY 745 cggaaacggtcacaatccaaagaggtctcagacacccctgagc 789
DB 2099 caaccagcctcaccagcaagcaggttctgtcagaccaccatgtgac 2143

RESULT 15
PCT-US02-10787-1
; Sequence 1, Application PC/TUS0210787
; GENERAL INFORMATION:
; APPLICANT: LEXICON GENETICS INCORPORATED
; TITLE OF INVENTION: Novel Human Kinase and Polynucleotides Encoding the Same
; FILE REFERENCE: LEX-0334-PCT
; CURRENT APPLICATION NUMBER: PCT/US02/10787
; PRIOR FILING DATE: 2002-04-04
; PRIOR APPLICATION NUMBER: US 60/282,031
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1158
; TYPE: DNA
; ORGANISM: homo sapiens
PCT-US02-10787-1

Query Match 12.4%; Score 97.8; DB 1; Length 1158;
Best Local Similarity 48.9%; Pred. No. 2.9e-16;
Matches 320; Conservative 0; Mismatches 332; Indels 3; Gaps 2;

QY 137 gggaggaatcgagcgaggtgtgagcatcctcggcaggtgtgtgacccaatgtcatca 196
DB 305 gagaagcgtgctgtctgagctgagctgtctcgtcgcggttagcatctgtatcatgtctc 364
QY 197 cgttcagagagctcatgtagaacgcgacgcagctgtgtgacatccttgagctagtgtctg 256
DB 365 agctatgtgagatcttctgagactgtgagatcaagtttaacatgtgtatgtgagctgtacgcg 424
QY 257 gaggagagcttgcattcctgtgcccagaagagatctagtgtgagaggggcacaca 316
DB 425 gagggagactcttgcagactcatctgtcagagatccttcaagagcggtatgcgta 484

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